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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

(ii) TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10

5 (iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA  
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15 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

20 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT  
(B) FILING DATE: 07-OCT-1994  
(C) CLASSIFICATION:

25 (viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: P-38,347  
(C) REFERENCE/DOCKET NUMBER: FD-3054 PCT

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30 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

5

(B) CLONE: NSC1

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10

CCGGAATTCA ARGTNGAYTT YGCNGAYATH GGNTGG

36

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: NSC2

20

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGGAATTCT CANGCRCARC TYTCNACNGT CAT

33

25

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vii) IMMEDIATE SOURCE:

(B) CLONE: NSC3

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..33

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGGAATTCT CANGCRCANG AYTACNACNGT CAT

33

(2) INFORMATION FOR SEQ ID NO:4:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2322 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20

(vii) IMMEDIATE SOURCE:

(B) CLONE: Murine GDF-10

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 126..1553

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGGGGTCATC CGGGCTGTCC GAGTCCCACA GGGACAACTC CAGCCGCGGA CGAGGTGCAC 60  
 AGCCAACACT GAGCCCTCCT TGTCTGTTCT CCTGGGCTCA GACCCTTCAC CACCGTTACT 120  
 5 CAGCC ATG GCT CCA GGT CCT GCT CGG ATC AGC TTG GGG TCC CAG CTG 167  
     Met Ala Pro Gly Pro Ala Arg Ile Ser Leu Gly Ser Gln Leu  
         1                    5                    10  
 CTG CCC ATG GTG CCG CTG CTC CTG CTG CTG CGG GGC GCA GGC TGC GGC 215  
 Leu Pro Met Val Pro Leu Leu Leu Leu Leu Arg Gly Ala Gly Cys Gly  
     15                    20                    25                    30  
 10 CAC AGG GGC CCC TCA TGG TCC TCA TTG CCC TCG GCA GCT GCC GGT CTG 263  
 His Arg Gly Pro Ser Trp Ser Ser Leu Pro Ser Ala Ala Ala Gly Leu  
                     35                    40                    45  
 CAG GGG GAC AGG GAC TCC CAG CAG TCA CCC GGG GAC GCA GCA GCC GCT 311  
 Gln Gly Asp Arg Asp Ser Gln Gln Ser Pro Gly Asp Ala Ala Ala Ala  
     15                    50                    55                    60  
 CTG GGC CCA GGC GCC CAG GAC ATG GTC GCT ATC CAC ATG CTC AGG CTC 359  
 Leu Gly Pro Gly Ala Gln Asp Met Val Ala Ile His Met Leu Arg Leu  
         65                    70                    75  
 20 TAT GAG AAG TAC AAC CGA AGA GGT GCT CCA CCG GGA GGA GGC AAC ACC 407  
 Tyr Glu Lys Tyr Asn Arg Arg Gly Ala Pro Pro Gly Gly Gly Asn Thr  
         80                    85                    90  
 GTC CGA AGC TTC CGT GCC CGG CTG GAA ATG ATC GAC CAA AAG CCT GTG 455  
 Val Arg Ser Phe Arg Ala Arg Leu Glu Met Ile Asp Gln Lys Pro Val  
     95                    100                    105                    110  
 25 TAT TTC TTC AAC TTG ACT TCC ATG CAA GAC TCA GAA ATG ATC CTC ACA 503  
 Tyr Phe Phe Asn Leu Thr Ser Met Gln Asp Ser Glu Met Ile Leu Thr  
                     115                    120                    125  
 GCC GCC TTC CAC TTC TAC TCA GAA CCT CCA CGG TGG CCC CGG GCT GGT 551  
 Ala Ala Phe His Phe Tyr Ser Glu Pro Pro Arg Trp Pro Arg Ala Gly  
     130                    135                    140  
 30 GAG GTA TTC TGC AAG CCC CGA GCT AAG AAC GCA TCC TGC CGC CTC CTG 599  
 Glu Val Phe Cys Lys Pro Arg Ala Lys Asn Ala Ser Cys Arg Leu Leu  
         145                    150                    155

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	ACC CCA GGG CTG CCT GCA CGC TTG CAC CTA ATC TTC CGC AGT CTT TCC Thr Pro Gly Leu Pro Ala Arg Leu His Leu Ile Phe Arg Ser Leu Ser 160 165 170	647
5	CAG AAC ACC GCC ACT CAG GGG CTG CTC CGC GGG GCC ATG GCC CTG ACG Gln Asn Thr Ala Thr Gln Gly Leu Leu Arg Gly Ala Met Ala Leu Thr 175 180 185 190	695
	CCT CCA CCA CGT GGC CTG TGG CAG GCC AAG GAC ATC TCC TCA ATC ATC Pro Pro Pro Arg Gly Leu Trp Gln Ala Lys Asp Ile Ser Ser Ile Ile 195 200 205	743
10	AAG GCT GCC CGA AGG GAT GGA GAG CTG CTT CTC TCT GCT CAG CTG GAT Lys Ala Ala Arg Arg Asp Gly Glu Leu Leu Leu Ser Ala Gln Leu Asp 215 220	791
15	ACT GAG AAG GAC CCC GGA GTG CCA CGG CCC AGT TCC CAC ATG CCC Thr Glu Lys Asp Pro Gly Val Pro Arg Pro Ser Ser His Met Pro 225 230 235	839
	TAT ATC CTT GTC TAC GCC AAT GAC CTG GCC ATC TCC GAA CCC AAC AGT Tyr Ile Leu Val Tyr Ala Asn Asp Leu Ala Ile Ser Glu Pro Asn Ser 240 245 250	887
20	GTA GCA GTG TCG CTA CAG AGA TAC GAC CCA TTT CCA GCT GGA GAC TTT Val Ala Val Ser Leu Gln Arg Tyr Asp Pro Phe Pro Ala Gly Asp Phe 255 260 265 270	935
	GAG CCT GGA GCA GCC CCC AAC AGC TCA GCT GAT CCC CGC GTG CGC AGG Glu Pro Gly Ala Ala Pro Asn Ser Ser Ala Asp Pro Arg Val Arg Arg 275 280 285	983
25	GCG GCT CAG GTG TCA AAA CCC CTG CAA GAC AAT GAA CTG CCG GGG CTG Ala Ala Gln Val Ser Lys Pro Leu Gln Asp Asn Glu Leu Pro Gly Leu 290 295 300	1031
30	GAT GAA AGA CCA GCG CCT GCC CTG CAT GCC CAG AAT TTC CAC AAG CAC Asp Glu Arg Pro Ala Pro Ala Leu His Ala Gln Asn Phe His Lys His 305 310 315	1079
	GAG TTC TGG TCC AGT CCT TTC CGG GCA CTG AAA CCC CGC ACG GCG CGC Glu Phe Trp Ser Ser Pro Phe Arg Ala Leu Lys Pro Arg Thr Ala Arg 320 325 330	1127

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	AAA GAC CGC AAG AAG AAG GAC CAG GAC ACA TTC ACC GCC GCC TCC TCT	1175
	Lys Asp Arg Lys Lys Lys Asp Gln Asp Thr Phe Thr Ala Ala Ser Ser	
	335 340 345 350	
5	CAG GTG CTG GAC TTT GAC GAG AAG ACG ATG CAG AAA GCC AGG AGG CGG	1223
	Gln Val Leu Asp Phe Asp Glu Lys Thr Met Gln Lys Ala Arg Arg Arg	
	355 360 365	
	CAG TGG GAT GAG CCC CGG GTC TGC TCC AGG AGG TAC CTG AAG GTG GAT	1271
	Gln Trp Asp Glu Pro Arg Val Cys Ser Arg Arg Tyr Leu Lys Val Asp	
	370 375 380	
10	TTT GCA GAC ATC GGG TGG AAT GAA TGG ATC ATC TCT CCC AAA TCC TTT	1319
	Phe Ala Asp Ile Gly Trp Asn Glu Trp Ile Ile Ser Pro Lys Ser Phe	
	385 390 395	
15	GAC GCC TAC TAC TGT GCT GGG GCC TGC GAG TTC CCC ATG CCC AAG ATT	1367
	Asp Ala Tyr Tyr Cys Ala Gly Ala Cys Glu Phe Pro Met Pro Lys Ile	
	400 405 410	
	GTC CGC CCA TCC AAC CAT GCC ACC ATC CAG AGC ATC GTC AGA GCT GTG	1415
	Val Arg Pro Ser Asn His Ala Thr Ile Gln Ser Ile Val Arg Ala Val	
	415 420 425 430	
20	GGC ATT GTC CCT GGC ATC CCA GAG CCA TGC TGT GTT CCA GAC AAG ATG	1463
	Gly Ile Val Pro Gly Ile Pro Glu Pro Cys Cys Val Pro Asp Lys Met	
	435 440 445	
	AAC TCC CTT GGA GTC CTT TTC CTG GAT GAA AAT CGG AAT GCG GTT CTG	1511
	Asn Ser Leu Gly Val Leu Phe Leu Asp Glu Asn Arg Asn Ala Val Leu	
	450 455 460	
25	AAG GTG TAC CCC AAT ATG TCC GTA GAG ACC TGT GCC TGT CGG	1553
	Lys Val Tyr Pro Asn Met Ser Val Glu Thr Cys Ala Cys Arg	
	465 470 475	
	TAAGATGGCT TCAAGATAGA AGACAGACCT GCTTCATCCC TGCCCTGCAG AGTGGCAATC	1613
	TTGGAGCCAG GGA CT T GACT CGGGGAGGTT CCAGGTGCTA GACAGAGCTT ACAGGCAGCC	1673
30	CTGCTGGGAC CAAGAAAGAT CTGCCCCACCA CATCGCAATT CTTCA GTTCT TCCGTGCTGG	1733
	TGGTAGCTCT GTAAAGACGT GTTGAGTTCC TGGAAGAAAT CTGGAATTAA CTGTGGTCTG	1793
	CAATTTGCCC ATCATCCCTG CCCACACTTT TCAAGGCCTA GAAATAACGT GTGTCCTCAA	1853

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ATGTCAACTC CAGGCATTTG TCCTCTCAAA ACCTAGAAAG ACTATGCAAA TCTTGGGGTA 1913  
 CTCCCCCCCC CCATGGCAGT TTAAATGCTG TTTTAAAACC CTCAGGCTGC ATTCTAGAAA 1973  
 CAGGGCCTAA CCCATGGCAC GAGTGAGTAT TTTCTCTTAC GTTTCACACTAC ACGTGCTTTT 2033  
 ATACATGCAG TATGCACATG TAATCACGGT TGATTTCTTC TTTTAATATA TGTATTTCTA 2093  
 5 TTTCAAAGCA AAACGGAGAG AGTCGATCCC ATCCCCTGCA GAGGTAATAA TGCAAGTTAG 2153  
 GTGTGGGGTTG TCTAAGCATG TGTATGGAAA TAATACATAC AGTAATATGC TGAATACTA 2213  
 AAAAAGTAAC CAAGATTTTA TATTTTGTGA AATTATACTT TGTATACTGT AGATTGTGAG 2273  
 TGTTCGTGT TTTTATGGAA AGCTAATAAA TTAAAGGTGC GGAGGTATC 2322

(2) INFORMATION FOR SEQ ID NO:5:

10

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Pro Gly Pro Ala Arg Ile Ser Leu Gly Ser Gln Leu Leu Pro  
 1 5 10 15

Met Val Pro Leu Leu Leu Leu Arg Gly Ala Gly Cys Gly His Arg  
 20 25 30

20

Gly Pro Ser Trp Ser Ser Leu Pro Ser Ala Ala Ala Gly Leu Gln Gly  
 35 40 45

Asp Arg Asp Ser Gln Gln Ser Pro Gly Asp Ala Ala Ala Leu Gly  
 50 55 60

25

Pro Gly Ala Gln Asp Met Val Ala Ile His Met Leu Arg Leu Tyr Glu  
 65 70 75 80

Lys Tyr Asn Arg Arg Gly Ala Pro Pro Gly Gly Gly Asn Thr Val Arg  
 85 90 95

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	Ser Phe Arg Ala Arg Leu Glu Met Ile Asp Gln Lys Pro Val Tyr Phe	
	100	105 110
	Phe Asn Leu Thr Ser Met Gln Asp Ser Glu Met Ile Leu Thr Ala Ala	
	115	120 125
5	Phe His Phe Tyr Ser Glu Pro Pro Arg Trp Pro Arg Ala Gly Glu Val	
	130	135 140
	Phe Cys Lys Pro Arg Ala Lys Asn Ala Ser Cys Arg Leu Leu Thr Pro	
	145	150 155 160
10	Gly Leu Pro Ala Arg Leu His Leu Ile Phe Arg Ser Leu Ser Gln Asn	
	165	170 175
	Thr Ala Thr Gln Gly Leu Leu Arg Gly Ala Met Ala Leu Thr Pro Pro	
	180	185 190
	Pro Arg Gly Leu Trp Gln Ala Lys Asp Ile Ser Ser Ile Ile Lys Ala	
	195	200 205
15	Ala Arg Arg Asp Gly Glu Leu Leu Leu Ser Ala Gln Leu Asp Thr Gly	
	210	215 220
	Glu Lys Asp Pro Gly Val Pro Arg Pro Ser Ser His Met Pro Tyr Ile	
	225	230 235 240
20	Leu Val Tyr Ala Asn Asp Leu Ala Ile Ser Glu Pro Asn Ser Val Ala	
	245	250 255
	Val Ser Leu Gln Arg Tyr Asp Pro Phe Pro Ala Gly Asp Phe Glu Pro	
	260	265 270
	Gly Ala Ala Pro Asn Ser Ser Ala Asp Pro Arg Val Arg Arg Ala Ala	
	275	280 285
25	Gln Val Ser Lys Pro Leu Gln Asp Asn Glu Leu Pro Gly Leu Asp Glu	
	290	295 300
	Arg Pro Ala Pro Ala Leu His Ala Gln Asn Phe His Lys His Glu Phe	
	305	310 315 320
30	Trp Ser Ser Pro Phe Arg Ala Leu Lys Pro Arg Thr Ala Arg Lys Asp	
	325	330 335



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Arg Lys Lys Lys Asp Gln Asp Thr Phe Thr Ala Ala Ser Ser Gln Val  
 340 345 350

Leu Asp Phe Asp Glu Lys Thr Met Gln Lys Ala Arg Arg Arg Gln Trp  
 355 360 365

5 Asp Glu Pro Arg Val Cys Ser Arg Arg Tyr Leu Lys Val Asp Phe Ala  
 370 375 380

Asp Ile Gly Trp Asn Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala  
 385 390 395 400

10 Tyr Tyr Cys Ala Gly Ala Cys Glu Phe Pro Met Pro Lys Ile Val Arg  
 405 410 415

Pro Ser Asn His Ala Thr Ile Gln Ser Ile Val Arg Ala Val Gly Ile  
 420 425 430

Val Pro Gly Ile Pro Glu Pro Cys Cys Val Pro Asp Lys Met Asn Ser  
 435 440 445

15 Leu Gly Val Leu Phe Leu Asp Glu Asn Arg Asn Ala Val Leu Lys Val  
 450 455 460

Tyr Pro Asn Met Ser Val Glu Thr Cys Ala Cys Arg  
 465 470 475

(2) INFORMATION FOR SEQ ID NO:6:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: GDF-10

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..120

30

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-1

(ix) FEATURE:

- (A) NAME/KEY: Protein  
(B) LOCATION: 1..123

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Arg Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Gly Pro Gly Gly  
 1 5 10 15  
 Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly Trp  
 5 20 25 30  
 His Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr Cys Gln  
 35 40 45  
 Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly Gly Pro Pro  
 50 55 60  
 Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala Ala Ala Pro  
 10 65 70 75 80  
 Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala Arg Leu Ser Pro Ile  
 85 90 95  
 Ser Val Leu Phe Phe Asp Asn Ser Asp Asn Val Val Leu Arg Gln Tyr  
 15 100 105 110  
 Glu Asp Met Val Val Asp Glu Cys Gly Cys Arg  
 115 120

(2) INFORMATION FOR SEQ ID NO:8:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: GDF-3

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..118

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Lys Arg Arg Ala Ala Ile Ser Val Pro Lys Gly Phe Cys Arg Asn  
 1 5 10 15  
 Phe Cys His Arg His Gln Leu Phe Ile Asn Phe Gln Asp Leu Gly Trp  
 5 20 25 30  
 His Lys Trp Val Ile Ala Pro Lys Gly Phe Met Ala Asn Tyr Cys His  
 35 40 45  
 Gly Glu Cys Pro Phe Ser Met Thr Thr Tyr Leu Asn Ser Ser Asn Tyr  
 50 55 60  
 Ala Phe Met Gln Ala Leu Met His Met Ala Asp Pro Lys Val Pro Lys  
 10 65 70 75 80  
 Ala Val Cys Val Pro Thr Lys Leu Ser Pro Ile Ser Met Leu Tyr Gln  
 85 90 95  
 Asp Ser Asp Lys Asn Val Ile Leu Arg His Tyr Glu Asp Met Val Val  
 15 100 105 110  
 Asp Glu Cys Gly Cys Gly  
 115

(2) INFORMATION FOR SEQ ID NO:9:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 119 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: GDF-9

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..119

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Phe Asn Leu Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn  
 1 5 10 15  
 5 Glu Cys Glu Leu His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp  
 20 25 30  
 Asp Asn Trp Ile Val Ala Pro His Arg Tyr Asn Pro Arg Tyr Cys Lys  
 35 40 45  
 Gly Asp Cys Pro Arg Ala Val Arg His Arg Tyr Gly Ser Pro Val His  
 50 55 60  
 10 Thr Met Val Gln Asn Ile Ile Tyr Glu Lys Leu Asp Pro Ser Val Pro  
 65 70 75 80  
 Arg Pro Ser Cys Val Pro Gly Lys Tyr Ser Pro Leu Ser Val Leu Thr  
 85 90 95  
 15 Ile Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile  
 100 105 110  
 Ala Thr Arg Cys Thr Cys Arg  
 115

## (2) INFORMATION FOR SEQ ID NO:10:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- 25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: BMP-2

- (ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..118

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Arg Glu Lys Arg Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser  
 1 5 10 15  
 Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp  
 5 20 25 30  
 Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His  
 35 40 45  
 Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His  
 50 55 60  
 Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys  
 10 65 70 75 80  
 Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu  
 85 90 95  
 Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val  
 15 100 105 110  
 Glu Gly Cys Gly Cys Arg  
 115

(2) INFORMATION FOR SEQ ID NO:11:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: BMP-4

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..118

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys  
 1 5 10 15  
 5 Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp  
 20 25 30  
 Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His  
 35 40 45  
 Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His  
 50 55 60  
 10 Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys  
 65 70 75 80  
 Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu  
 85 90 95  
 15 Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val  
 100 105 110  
 Glu Gly Cys Gly Cys Arg  
 115

(2) INFORMATION FOR SEQ ID NO:12:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 119 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: Vgr-1

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..119

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Arg Gly Ser Gly Ser Ser Asp Tyr Asn Gly Ser Glu Leu Lys Thr  
 1 5 10 15  
 5 Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp  
 20 25 30  
 Gln Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp  
 35 40 45  
 Gly Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His  
 50 55 60  
 10 Ala Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro  
 65 70 75 80  
 Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr  
 85 90 95  
 15 Phe Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val  
 100 105 110  
 Val Arg Ala Cys Gly Cys His  
 115

(2) INFORMATION FOR SEQ ID NO:13:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 119 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: OP-1

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..119



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln
1              5                      10                      15

Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp
5              20                      25                      30

Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu
              35                      40                      45

Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His
              50                      55                      60

Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr Val Pro
10             65                      70                      75                      80

Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val Leu Tyr
              85                      90                      95

Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val
15             100                     105                     110

Val Arg Ala Cys Gly Cys His
              115

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(2) INFORMATION FOR SEQ ID NO:14:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:  
(B) CLONE: BMP-5

```
(ix) FEATURE:
      (A) NAME/KEY: Protein
      (B) LOCATION: 1..119
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15

Val Arg Ser Cys Gly Cys His  
115

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:

- (B) CLONE: OP-2

(ix) FEATURE:

- (A) NAME/KEY: Protein  
(B) LOCATION: 1..119

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln  
 1 5 10 15  
 Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp  
 5 20 25 30  
 Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu  
 35 40 45  
 Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His  
 50 55 60  
 Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro  
 10 65 70 75 80  
 Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr  
 85 90 95  
 Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys Ala Arg Asn Met Val  
 15 100 105 110  
 Val Lys Ala Cys Gly Cys His  
 115

## (2) INFORMATION FOR SEQ ID NO:16:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: BMP-3

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..120

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Gln Thr Leu Lys Lys Ala Arg Arg Lys Gln Trp Ile Glu Pro Arg  
 1 5 10 15  
 Asn Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp  
 5 20 25 30  
 Ser Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser  
 35 40 45  
 Gly Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His  
 50 55 60  
 Ala Thr Ile Gln Ser Ile Val Arg Ala Val Gly Val Val Pro Gly Ile  
 10 65 70 75 80  
 Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu  
 85 90 95  
 Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met  
 15 100 105 110  
 Thr Val Glu Ser Cys Ala Cys Arg  
 115 120

## (2) INFORMATION FOR SEQ ID NO:17:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: MIS

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..116

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Pro Gly Arg Ala Gln Arg Ser Ala Gly Ala Thr Ala Ala Asp Gly  
 1 5 10 15  
 5 Pro Cys Ala Leu Arg Glu Leu Ser Val Asp Leu Arg Ala Glu Arg Ser  
 20 25 30  
 Val Leu Ile Pro Glu Thr Tyr Gln Ala Asn Asn Cys Gln Gly Val Cys  
 35 40 45  
 Gly Trp Pro Gln Ser Asp Arg Asn Pro Arg Tyr Gly Asn His Val Val  
 50 55 60  
 10 Leu Leu Leu Lys Met Gln Ala Arg Gly Ala Ala Leu Ala Arg Pro Pro  
 65 70 75 80  
 Cys Cys Val Pro Thr Ala Tyr Ala Gly Lys Leu Leu Ile Ser Leu Ser  
 85 90 95  
 15 Glu Glu Arg Ile Ser Ala His His Val Pro Asn Met Val Ala Thr Glu  
 100 105 110  
 Cys Gly Cys Arg  
 115

(2) INFORMATION FOR SEQ ID NO:18:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 122 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: Inhibin-alpha

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..122

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Leu Arg Leu Leu Gln Arg Pro Pro Glu Glu Pro Ala Ala His Ala  
 1 5 10 15

5 Asn Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu Leu Gly Trp  
 20 25 30

Glu Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His Tyr Cys His  
 35 40 45

Gly Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu Pro Val Pro  
 50 55 60

10 Gly Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu Pro Gly Ala  
 65 70 75 80

Gln Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro Leu His Val  
 85 90 95

15 Arg Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu Thr Val Pro  
 100 105 110

Asn Leu Leu Thr Gln His Cys Ala Cys Ile  
 115 120

## (2) INFORMATION FOR SEQ ID NO:19:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein.

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: Inhibin-beta-A

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..121

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Arg Arg Arg Arg Arg Gly Leu Glu Cys Asp Gly Lys Val Asn Ile Cys  
 1 5 10 15  
 5 Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn Asp  
 20 25 30  
 Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly Glu  
 35 40 45  
 Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe His  
 50 55 60  
 10 Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe Ala  
 65 70 75 80  
 Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser Met  
 85 90 95  
 15 Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln Asn  
 100 105 110  
 Met Ile Val Glu Glu Cys Gly Cys Ser  
 115 120

(2) INFORMATION FOR SEQ ID NO:20:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: Inhibin-beta-B

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..120

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg Ile Arg Lys Arg Gly Leu Glu Cys Asp Gly Arg Thr Asn Leu Cys  
 1 5 10 15  
 5 Cys Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn Asp  
 20 25 30  
 Trp Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly Ser  
 35 40 45  
 Cys Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe His  
 50 55 60  
 10 Thr Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly Thr  
 65 70 75 80  
 Val Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met Leu  
 85 90 95  
 15 Tyr Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn Met  
 100 105 110  
 Ile Val Glu Glu Cys Gly Cys Ala  
 115 120

(2) INFORMATION FOR SEQ ID NO:21:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: Nodal

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..118



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Trp Gly Arg Arg Gln Arg Arg His His Leu Pro Asp Arg Ser Gln  
 1                      5                      10                      15  
 5      Leu Cys Arg Arg Val Lys Phe Gln Val Asp Phe Asn Leu Ile Gly Trp  
                     20                      25                      30  
 Gly Ser Trp Ile Ile Tyr Pro Lys Gln Tyr Asn Ala Tyr Arg Cys Glu  
                     35                      40                      45  
 Gly Glu Cys Pro Asn Pro Val Gly Glu Glu Phe His Pro Thr Asn His  
                     50                      55                      60  
 10      Ala Tyr Ile Gln Ser Leu Leu Lys Arg Tyr Gln Pro His Arg Val Pro  
                     65                      70                      75                      80  
 Ser Thr Cys Cys Ala Pro Val Lys Thr Lys Pro Leu Ser Met Leu Tyr  
                     85                      90                      95  
 15      Val Asp Asn Gly Arg Val Leu Leu Glu His His Lys Asp Met Ile Val  
                     100                      105                      110  
 Glu Glu Cys Gly Cys Leu  
                     115

(2) INFORMATION FOR SEQ ID NO:22:

20      (i) SEQUENCE CHARACTERISTICS:  
             (A) LENGTH: 114 amino acids  
             (B) TYPE: amino acid  
             (C) STRANDEDNESS: single  
             (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25      (vii) IMMEDIATE SOURCE:  
             (B) CLONE: TGF-beta-1

(ix) FEATURE:  
             (A) NAME/KEY: Protein  
             (B) LOCATION: 1..114

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn  
 1 5 10 15  
 5 Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp  
 20 25 30  
 Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly  
 35 40 45  
 Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu  
 50 55 60  
 10 Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys  
 65 70 75 80  
 Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg  
 85 90 95  
 15 Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys  
 100 105 110  
 Cys Ser

## (2) INFORMATION FOR SEQ ID NO:23:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 114 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: TGF-beta-2

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..114

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Lys Arg Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn  
 1 5 10 15  
 Cys Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp  
 5 20 25 30  
 Lys Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly  
 35 40 45  
 Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu  
 50 55 60  
 Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys  
 10 65 70 75 80  
 Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys  
 85 90 95  
 Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys  
 15 100 105 110  
 Cys Ser

## (2) INFORMATION FOR SEQ ID NO:24:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 114 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein
- 25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: TGF-beta-3  
 (ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..114

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Lys Arg Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn  
 1 5 10 15  
 Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp  
 5 20 25 30  
 Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly  
 35 40 45  
 Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu  
 50 55 60  
 Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys  
 10 65 70 75 80  
 Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg  
 85 90 95  
 Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys  
 15 100 105 110  
 Cys Ser

## (2) INFORMATION FOR SEQ ID NO:25:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: Human GDF-10

(ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..115

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Lys Ala Arg Arg Lys Gln Trp Asp Glu Pro Arg Val Cys Ser Arg Arg  
 1 5 10 15  
 Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Asn Glu Trp Ile Ile  
 5 20 25 30  
 Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ala Gly Ala Cys Glu Phe  
 35 40 45  
 Pro Met Pro Lys Ile Val Arg Pro Ser Asn His Ala Thr Ile Gln Ser  
 50 55 60  
 Ile Val Arg Ala Val Gly Ile Ile Pro Gly Ile Pro Glu Pro Cys Cys  
 10 65 70 75 80  
 Val Pro Asp Lys Met Asn Ser Leu Gly Val Leu Phe Leu Asp Glu Asn  
 85 90 95  
 Arg Asn Val Val Leu Lys Val Tyr Pro Asn Met Ser Val Asp Thr Cys  
 15 100 105 110  
 Ala Cys Arg  
 115

## (2) INFORMATION FOR SEQ ID NO:26:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: protein  
  
 25 (vii) IMMEDIATE SOURCE:  
 (B) CLONE: Murine GDF-10  
  
 (ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..115

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys Ala Arg Arg Lys Gln Trp Asp Glu Pro Arg Val Cys Ser Arg Arg  
1 5 10 15

5 Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Asn Glu Trp Ile Ile  
20 25 30

Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ala Gly Ala Cys Glu Phe  
35 40 45

Pro Met Pro Lys Ile Val Arg Pro Ser Asn His Ala Thr Ile Gln Ser  
50 55 60

10 Ile Val Arg Ala Val Gly Ile Val Pro Gly Ile Pro Glu Pro Cys Cys  
65 70 75 80

Val Pro Asp Lys Met Asn Ser Leu Gly Val Leu Phe Leu Asp Glu Asn  
85 90 95

15 Arg Asn Ala Val Leu Lys Val Tyr Pro Asn Met Ser Val Glu Thr Cys  
100 105 110

Ala Cys Arg  
115